

RAW SEQUENCE LISTING

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Application Serial Number: 10/528,748
Source: PCT
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/528,748

DATE: 03/30/2005
TIME: 14:14:12

Input Set : A:\NHL-NP-49-NP.ST25.txt
Output Set: N:\CRF4\03302005\J528748.raw

3 <110> APPLICANT: JUNGHANS, Claas
4 SCHROFF, Matthias
5 JUHLS, Christiane
6 OSWALD, Detlef
8 <120> TITLE OF INVENTION: Vaccine against Oncovirus Infections, such as infections by
9 Feline leukosis virus of the cat
11 <130> FILE REFERENCE: NHL-NP-49-NP
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,748
C--> 13 <141> CURRENT FILING DATE: 2005-03-22
13 <150> PRIOR APPLICATION NUMBER: DE 102 44 863.9
14 <151> PRIOR FILING DATE: 2002-09-23
16 <150> PRIOR APPLICATION NUMBER: PCT/DE2003/003179
17 <151> PRIOR FILING DATE: 2003-09-19
19 <160> NUMBER OF SEQ ID NOS: 40
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1929
25 <212> TYPE: DNA
26 <213> ORGANISM: Feline leukemia virus
29 <220> FEATURE:
30 <221> NAME/KEY: gene
31 <222> LOCATION: (1)..(1929)
32 <223> OTHER INFORMATION: DNA sequence wild type "env" gene without signal peptide
coding
33 region
35 <300> PUBLICATION INFORMATION:
36 <308> DATABASE ACCESSION NO: NCBI M12500
37 <309> DATABASE ENTRY DATE: 2001-02-21
38 <313> RELEVANT RESIDUES: (162)..(1990)
40 <400> SEQUENCE: 1
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43 tttctgggtgg ggtatcttatt tacaatagac ataggaatgg ccaatcctag tcccacccaa 120
45 atatataatg taacttgggt aataaccaat gtacaaacta acacccaagc taacgccacc 180
47 tctatgttag gaaccttaac cgatgcctac cctaccctac atgttgactt atgtgaccta 240
49 gtgggagaca cctgggaaacc tatagtccctaa aacccaaacca atgtaaaaca cggggcacgt 300
51 tactcctctt caaaatatgg atgtaaaact acagataaaaaaaaacacagca acagacatac 360
53 cccttttacg tctgccccgg acatgcccccc tcgttggggc caaaggaaac acattgtgga 420
55 ggggcacaag atgggttttg tgccgcattgg ggatgtgaga ccacccggaga agcttgggtgg 480
57 aagcccacccct cctcatggta ctatatcaca gtaaaaagag ggagtagtca ggacaatagc 540
59 tgtgagggaa aatgcaaccc cctgggttttg cagttcaccc agaaggaaag acaaggctct 600
61 tgggacggac ctaagatgtg gggattgcga ctataccgtc caggatatga ccctatcgct 660
63 ttattcacgg tggccggca ggtatcaacc attacggccgc ctcaggcaat gggaccaaac 720
65 ctagtcttac ctgatcaaaaa acccccatcc cgacaatctc aaacagggtc caaagtggcg 780
67 acccagagggc cccaaacgaa tggaaagcgcc ccaaggctcg ttgcccccac caccatgggt 840

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73	ccctattacg	aagggattgc	aatcttaggt	aactacagca	acccaaacaaa	ccccccccc	1020
75	tcctgcctat	ctactccgca	acacaaacta	actatatctg	aagtatcagg	gcaaggaatg	1080
77	tgcataggga	ctgttcccaa	aacccaccag	gctttgtca	ataagacaca	acagggacat	1140
79	acaggggcgc	actatctagc	cgcccccaac	ggcacctatt	gggcctgtaa	cactggactc	1200
81	accccatgca	tttccatggc	ggtgctcaat	tggacctctg	attttgcgt	cttaatcgaa	1260
83	ttatggccca	gagtgactta	ccatcaaccc	gaataatgtgt	acacacattt	tgccaaagct	1320
85	gtcaggttcc	gaagagaacc	aatatcacta	acggttccc	ttatgttggg	aggacttact	1380
87	gtagggggca	tagccgcggg	ggtcggaaaca	gggactaaag	ccctccttga	aacagcccg	1440
89	ttcagacaac	tacaaatggc	catgcacaca	gacatccagg	ccctagaaga	atcaattagt	1500
91	gccttagaaa	agtccctgac	ctccctttct	gaagtagtct	tacaaaacag	acggggccta	1560
93	gatattctat	tcttacaaga	gggagggctc	tgtccgcatt	tgaaagaaga	atgttgcttc	1620
95	tatgcggatc	acaccggact	cgtccgagac	aatatggca	aattaagaga	aagactaaaa	1680
97	cagcggcaac	aactgtttga	ctcccaacag	ggatgtttt	aaggatggtt	caacaagtcc	1740
99	ccctggttta	caaccctaat	ttcctccatt	atggggccct	tactaatct	actcctaatt	1800
101	ctccttctcg	gcccatgcat	ccttaaccga	ttagtacaat	tcgtaaaaga	cagaatatct	1860
103	gtggtacagg	ctttaatttt	aacccaacag	taccaacaga	taaagcaata	cgatccggac	1920
105	cgaccatga						1929
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109	<211>	LENGTH:	1527				
110	<212>	TYPE:	DNA				
111	<213>	ORGANISM:	Feline leukemia virus				
114	<220>	FEATURE:					
115	<221>	NAME/KEY:	gene				
116	<222>	LOCATION:	(1)..(1527)				
117	<223>	OTHER INFORMATION:	DNA sequence wild type "gag" gene				
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124	gccgaatggg	taatgatgaa	tgtaggttgg	ccccgagaag	gaactttcac	cattgacaat	180
126	atttcacagg	tcgaggagag	aatcttcgc	ccggggccat	atggacacccc	agatcaaattc	240
128	ccttatatta	ccacgtggag	atccctagcc	acagacccccc	ctccatgggt	tcgcccattc	300
130	ctaccccttc	ctaagcatcc	caggacagat	cctcccgac	ctcttcgccc	gcaaccttct	360
132	gcccgcac	cctctccccc	ccaccccgcc	ctctaccccg	ttctcccaaa	accagacccc	420
134	cccaaggcgc	ctgttattacc	acccaatcct	tcttccctt	taattgtatc	cttaacagaa	480
136	gagccaccc	cctatccgg	gggtcacggg	ccaaacaccgc	cgtcaggccc	tagaacccca	540
138	actgcctccc	cgattccat	ccggctgcga	gaacgacgag	aaaatccagc	tgagaaatct	600
140	caagccctcc	ccttaaggga	agacccaaac	aacagacccc	agtactggcc	attctcgccc	660
142	tctgacctgt	acaattggaa	attgcataac	ccccctttct	cccaggaccc	agtggcccta	720
144	actaacctaa	ttgagtccat	tttagtgcaca	catcagccaa	cctgggacga	ctgccaacag	780
146	ctcttacagg	ctctcctgac	ggcagaggag	agacaaaggg	tcctccttga	agccccaaag	840
148	caagttccag	gcgaggacgg	acggccaacc	cagctccca	atgtcgttgc	cgaggcttc	900
150	cccttgcacc	gtcccaactg	ggatttttgt	acgccccggc	gtagggagca	cctacgcctt	960
152	tatgccagt	tgctgttagc	ggggctccgc	ggggctgcac	gacgccccac	taatttggca	1020
154	caggtaaagc	aagttgtaca	agggaaagag	gaaacgcac	cctcattttt	agaaagatta	1080
156	aaagaggctt	acagaatgtt	tactccctat	gaccctgagg	acccaggggca	ggctgctagt	1140
158	gttatccctgt	cctttatcta	ccagtctagc	ccggacataaa	gaaataagtt	acaaaggctt	1200
160	gaaggcctac	agggggttac	actgtctgtat	ttgctaaaag	aggcagaaaa	gatataacaac	1260

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162	aaaaggaaaa	ccccagagga	aaggaaagaa	agattatggc	agcggcagga	agaaaagagat	1320										
164	aaaaagcgcc	ataaggagat	gactaaagt	ctggccacag	tagtgctca	gaatagagat	1380										
166	aaggatagag	gggaaagtaa	actgggagat	caaaggaaaa	tacctctggg	gaaagaccag	1440										
168	tgtgcctatt	gcaaggaaaa	gggacatttg	gttcgcattt	gccccgaaacg	accccgaaag	1500										
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173	<210>	SEQ ID NO:	3														
174	<211>	LENGTH:	642														
175	<212>	TYPE:	PRT														
176	<213>	ORGANISM:	Feline leukemia virus														
179	<220>	FEATURE:															
180	<221>	NAME/KEY:	PEPTIDE														
181	<222>	LOCATION:	(1)..(447)														
182	<223>	OTHER INFORMATION:	Amino acid sequence of the protein corresponding to Seq.ID1														
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187	1						5							10			15
190	Trp	Asn	Leu	Ala	Phe	Leu	Val	Gly	Ile	Leu	Phe	Thr	Ile	Asp	Ile	Gly	
191								20				25			30		
194	Met	Ala	Asn	Pro	Ser	Pro	His	Gln	Ile	Tyr	Asn	Val	Thr	Trp	Val	Ile	
195								35			40			45			
198	Thr	Asn	Val	Gln	Thr	Asn	Thr	Gln	Ala	Asn	Ala	Thr	Ser	Met	Leu	Gly	
199								50			55			60			
202	Thr	Leu	Thr	Asp	Ala	Tyr	Pro	Thr	Leu	His	Val	Asp	Leu	Cys	Asp	Leu	
203	65						65				70			75		80	
206	Val	Gly	Asp	Thr	Trp	Glu	Pro	Ile	Val	Leu	Asn	Pro	Thr	Asn	Val	Lys	
207								85			90			95			
210	His	Gly	Ala	Arg	Tyr	Ser	Ser	Ser	Lys	Tyr	Gly	Cys	Lys	Thr	Thr	Asp	
211								100			105			110			
214	Arg	Lys	Gln	Gln	Gln	Thr	Tyr	Pro	Phe	Tyr	Val	Cys	Pro	Gly	His		
215							115			120			125				
218	Ala	Pro	Ser	Leu	Gly	Pro	Lys	Gly	Thr	His	Cys	Gly	Gly	Ala	Gln	Asp	
219							130			135			140				
222	Gly	Phe	Cys	Ala	Ala	Trp	Gly	Cys	Glu	Thr	Thr	Gly	Glu	Ala	Trp	Trp	
223	145						145			150			155			160	
226	Lys	Pro	Thr	Ser	Ser	Trp	Asp	Tyr	Ile	Thr	Val	Lys	Arg	Gly	Ser	Ser	
227								165			170			175			
230	Gln	Asp	Asn	Ser	Cys	Glu	Gly	Lys	Cys	Asn	Pro	Leu	Val	Leu	Gln	Phe	
231							180			185			190				
234	Thr	Gln	Lys	Gly	Arg	Gln	Ala	Ser	Trp	Asp	Gly	Pro	Lys	Met	Trp	Gly	
235							195			200			205				
238	Leu	Arg	Leu	Tyr	Arg	Thr	Gly	Tyr	Asp	Pro	Ile	Ala	Leu	Phe	Thr	Val	
239							210			215			220				
242	Ser	Arg	Gln	Val	Ser	Thr	Ile	Thr	Pro	Pro	Gln	Ala	Met	Gly	Pro	Asn	
243	225						225			230			235			240	
246	Leu	Val	Leu	Pro	Asp	Gln	Lys	Pro	Pro	Ser	Arg	Gln	Ser	Gln	Thr	Gly	
247							245			250			255				
250	Ser	Lys	Val	Ala	Thr	Gln	Arg	Pro	Gln	Thr	Asn	Glu	Ser	Ala	Pro	Arg	
251							260			265			270				
254	Ser	Val	Ala	Pro	Thr	Thr	Met	Gly	Pro	Lys	Arg	Ile	Gly	Thr	Gly	Asp	

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255	275	280	285
258	Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala Leu Asn Ala Thr		
259	290	295	300
262	Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro		
263	305	310	315
266	320	325	335
267	330	335	
270	Asn Pro Pro Pro Ser Cys Leu Ser Thr Pro Gln His Lys Leu Thr Ile		
271	340	345	350
274	Ser Glu Val Ser Gly Gln Gly Met Cys Ile Gly Thr Val Pro Lys Thr		
275	355	360	365
278	His Gln Ala Leu Cys Asn Lys Thr Gln Gln Gly His Thr Gly Ala His		
279	370	375	380
282	Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu		
283	385	390	395
286	400	405	415
287	Thr Pro Cys Ile Ser Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys		
290	410	420	430
291	425	430	
294	Val Tyr Thr His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile		
295	435	440	445
298	445	450	460
299	455	460	
302	Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln		
303	465	470	475
306	480	485	495
307	490	495	
310	Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu		
311	500	505	510
314	510	515	525
315	520	525	
318	Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His		
319	530	535	540
322	540	545	560
323	550	555	
326	560	565	575
327	570	575	
330	Phe Asn Lys Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly		
331	580	585	590
334	590	595	605
335	605	610	
338	610	615	620
339	620	630	
342	635	640	
346	Arg Pro		
350	<210> SEQ ID NO: 4		
351	<211> LENGTH: 508		
352	<212> TYPE: PRT		

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353 <213> ORGANISM: Feline leukemia virus
 356 <220> FEATURE:
 357 <221> NAME/KEY: PEPTIDE
 358 <222> LOCATION: (1)..(508)
 359 <223> OTHER INFORMATION: Amino acid sequence of the protein corresponding to Seq.ID2
 361 <400> SEQUENCE: 4
 363 Met Gly Gln Thr Ile Thr Thr Pro Leu Ser Leu Thr Leu Asn His Trp
 364 1 5 10 15
 367 Ser Glu Val Gln Ala Arg Ala Arg Asn Gln Gly Val Glu Val Arg Lys
 368 20 25 30
 371 Lys Lys Trp Ile Thr Leu Cys Glu Ala Glu Trp Val Met Met Asn Val
 372 35 40 45
 375 Gly Trp Pro Arg Glu Gly Thr Phe Thr Ile Asp Asn Ile Ser Gln Val
 376 50 55 60
 379 Glu Glu Arg Ile Phe Ala Pro Gly Pro Tyr Gly His Pro Asp Gln Ile
 380 65 70 75 80
 383 Pro Tyr Ile Thr Thr Trp Arg Ser Leu Ala Thr Asp Pro Pro Pro Trp
 384 85 90 95
 387 Val Arg Pro Phe Leu Pro Pro Pro Lys His Pro Arg Thr Asp Pro Pro
 388 100 105 110
 391 Glu Pro Leu Ser Pro Gln Pro Leu Ala Pro Gln Pro Ser Ser Pro His
 392 115 120 125
 395 Pro Val Leu Tyr Pro Val Leu Pro Lys Pro Asp Pro Pro Lys Ala Pro
 396 130 135 140
 399 Val Leu Pro Pro Asn Pro Ser Ser Pro Leu Ile Asp Leu Leu Thr Glu
 400 145 150 155 160
 403 Glu Pro Pro Pro Tyr Pro Gly Gly His Gly Pro Thr Pro Pro Ser Gly
 404 165 170 175
 407 Pro Arg Thr Pro Thr Ala Ser Pro Ile Ala Ile Arg Leu Arg Glu Arg
 408 180 185 190
 411 Arg Glu Asn Pro Ala Glu Lys Ser Gln Ala Leu Pro Leu Arg Glu Asp
 412 195 200 205
 415 Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe Ser Ala Ser Asp Leu Tyr
 416 210 215 220
 419 Asn Trp Lys Leu His Asn Pro Pro Phe Ser Gln Asp Pro Val Ala Leu
 420 225 230 235 240
 423 Thr Asn Leu Ile Glu Ser Ile Leu Val Thr His Gln Pro Thr Trp Asp
 424 245 250 255
 427 Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu Thr Ala Glu Glu Arg Gln
 428 260 265 270
 431 Arg Val Leu Leu Glu Ala Arg Lys Gln Val Pro Gly Glu Asp Gly Arg
 432 275 280 285
 435 Pro Thr Gln Leu Pro Asn Val Val Asp Glu Ala Phe Pro Leu Thr Arg
 436 290 295 300
 439 Pro Asn Trp Asp Phe Cys Thr Pro Ala Gly Arg Glu His Leu Arg Leu
 440 305 310 315 320
 443 Tyr Arg Gln Leu Leu Ala Gly Leu Arg Gly Ala Ala Arg Arg Pro
 444 325 330 335
 447 Thr Asn Leu Ala Gln Val Lys Gln Val Val Gln Gly Lys Glu Glu Thr

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date